

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/525,178  
Source: PCT  
Date Processed by STIC: 06/29/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/525,178

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4      Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)             . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi)  SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."  
                          Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa     "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



PCT

## RAW SEQUENCE LISTING

DATE: 06/29/2006

PATENT APPLICATION: US/10/525,178

TIME: 10:17:34

Input Set : A:\73975\_SEQLIST.txt

Output Set: N:\CRF4\06292006\J525178.raw

3 <110> APPLICANT: Emanuel Hanski  
 4 Allon E. Moses  
 5 Carlos Hidalgo-Grass  
 7 <120> TITLE OF INVENTION: Compositions And Methods For Treatment And Prophylaxis Of  
 8 Infections Caused By Gram Positive Bacteria  
 10 <130> FILE REFERENCE: 73975/JPW/JW; 14975-WO-02  
 12 <140> CURRENT APPLICATION NUMBER: US 10/525,178  
 C--> 13 <141> CURRENT FILING DATE: 2005-02-22  
 15 <150> PRIOR APPLICATION NUMBER: PCT/IL03/00687  
 16 <151> PRIOR FILING DATE: 2003-08-19  
 18 <150> PRIOR APPLICATION NUMBER: IL 151436  
 19 <151> PRIOR FILING DATE: 2002-08-22  
 21 <160> NUMBER OF SEQ ID NOS: 32  
 23 <170> SOFTWARE: PatentIn version 3.3  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 19  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Artificial Sequence  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: m13/puc sequence primer (-20)  
 33 <400> SEQUENCE: 1  
 34 gtaaaaaaacg acggccagt 19  
 37 <210> SEQ ID NO: 2  
 38 <211> LENGTH: 16  
 39 <212> TYPE: DNA  
 40 <213> ORGANISM: Artificial Sequence  
 42 <220> FEATURE:  
 43 <223> OTHER INFORMATION: m13/puc reverse sequencing primer (-21) forward primer for  
 tag  
 44 amplification  
 46 <400> SEQUENCE: 2  
 47 aacagctatg accatg 16  
 50 <210> SEQ ID NO: 3  
 51 <211> LENGTH: 20  
 52 <212> TYPE: DNA  
 53 <213> ORGANISM: Artificial Sequence  
 55 <220> FEATURE:  
 56 <223> OTHER INFORMATION: Reverse primer for tag amplification  
 58 <400> SEQUENCE: 3  
 59 agcagttcgt agttatcttg 20  
 62 <210> SEQ ID NO: 4  
 63 <211> LENGTH: 19  
 64 <212> TYPE: DNA  
 65 <213> ORGANISM: Artificial Sequence

Does Not Comply  
Corrected Diskette Needed

Cpg-4)

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Input Set : A:\73975\_SEQLIST.txt

Output Set: N:\CRF4\06292006\J525178.raw

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67 <220> FEATURE:
68 <223> OTHER INFORMATION: Inverse PCR primer from IRr
70 <400> SEQUENCE: 4
71 ttatcagcaa taaaccagc 19
74 <210> SEQ ID NO: 5
75 <211> LENGTH: 18
76 <212> TYPE: DNA
77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: Inverse primer from IR1
82 <400> SEQUENCE: 5
83 aaagtccctcc tgggtatg 18
86 <210> SEQ ID NO: 6
87 <211> LENGTH: 20
88 <212> TYPE: DNA
89 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: Inverse PCR primer from 3' of sile
94 <400> SEQUENCE: 6
95 tttggcagct ttgacgatgc 20
98 <210> SEQ ID NO: 7
99 <211> LENGTH: 20
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Inverse PCR primer from 5' of Sila
106 <400> SEQUENCE: 7
107 tcttcaagca gctgattggg 20
110 <210> SEQ ID NO: 8
111 <211> LENGTH: 23
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: 2598-2620 in sil
118 <400> SEQUENCE: 8
119 ggagttggtt tatcaaagt cag 23
122 <210> SEQ ID NO: 9
123 <211> LENGTH: 23
124 <212> TYPE: DNA
125 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: 3213-3235 in sil
130 <400> SEQUENCE: 9
131 atctgccaca aagactgatc aag 23
134 <210> SEQ ID NO: 10
135 <211> LENGTH: 21
136 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:

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## RAW SEQUENCE LISTING

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DATE: 06/29/2006

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Input Set : A:\73975\_SEQLIST.txt

Output Set: N:\CRF4\06292006\J525178.raw

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140 <223> OTHER INFORMATION: 2013-2033 in sil
142 <400> SEQUENCE: 10
143 ttattggatc ggaacttacg c 21
146 <210> SEQ ID NO: 11
147 <211> LENGTH: 21
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: 3554-3574 in sil
154 <400> SEQUENCE: 11
155 tgcttcccaa caacttacca c 21
158 <210> SEQ ID NO: 12
159 <211> LENGTH: 22
160 <212> TYPE: DNA
161 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: 2088-2109 in sil
166 <400> SEQUENCE: 12
167 gctcgctata gtaagcaa at cg 22
170 <210> SEQ ID NO: 13
171 <211> LENGTH: 18
172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <223> OTHER INFORMATION: 5871-5888 in sil
178 <400> SEQUENCE: 13
179 cagcgattaa gcattgac 18
182 <210> SEQ ID NO: 14
183 <211> LENGTH: 20
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: 1616-1634 in sil
190 <400> SEQUENCE: 14
191 acgaaaggtc aatggttcac 20
194 <210> SEQ ID NO: 15
195 <211> LENGTH: 20
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: 2338-2357 in sil
202 <400> SEQUENCE: 15
203 aggtatggat aagcgttgag 20
206 <210> SEQ ID NO: 16
207 <211> LENGTH: 20
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: 3873-3894 in sil

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## RAW SEQUENCE LISTING

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Input Set : A:\73975\_SEQLIST.txt

Output Set: N:\CRF4\06292006\J525178.raw

214 <400> SEQUENCE: 16  
 215 atgacacttg ttacacgtcc  
 218 <210> SEQ ID NO: 17  
 219 <211> LENGTH: 22  
 220 <212> TYPE: DNA  
 221 <213> ORGANISM: Artificial Sequence  
 223 <220> FEATURE:  
 224 <223> OTHER INFORMATION: 3873-3984  
 226 <400> SEQUENCE: 17  
 227 actagtcagc ttgacgaact tc  
 230 <210> SEQ ID NO: 18  
 231 <211> LENGTH: 19  
 232 <212> TYPE: DNA  
 233 <213> ORGANISM: Artificial Sequence  
 235 <220> FEATURE:  
 236 <223> OTHER INFORMATION: emm typing forward primer  
 238 <400> SEQUENCE: 18  
 239 tattcgctta gaaaattaa  
 242 <210> SEQ ID NO: 19  
 243 <211> LENGTH: 20  
 244 <212> TYPE: DNA  
 245 <213> ORGANISM: Artificial Sequence  
 247 <220> FEATURE:  
 248 <223> OTHER INFORMATION: emm typing reverse primer  
 250 <400> SEQUENCE: 19  
 251 gcaagttctt cagcttggtt  
 254 <210> SEQ ID NO: 20  
 255 <211> LENGTH: 28  
 256 <212> TYPE: DNA  
 257 <213> ORGANISM: Artificial Sequence  
 259 <220> FEATURE:  
 260 <223> OTHER INFORMATION: aad9 forward primer  
 262 <400> SEQUENCE: 20  
 263 ccattggtcct cgagctctag atcttaag  
 266 <210> SEQ ID NO: 21  
 267 <211> LENGTH: 25  
 268 <212> TYPE: DNA  
 269 <213> ORGANISM: Artificial Sequence  
 271 <220> FEATURE:  
 272 <223> OTHER INFORMATION: aad9 reverse primer  
 274 <400> SEQUENCE: 21  
 275 ctgcaggcgc ttaccaatta gaatg  
 278 <210> SEQ ID NO: 22  
 279 <211> LENGTH: 24  
 280 <212> TYPE: DNA  
 281 <213> ORGANISM: Artificial Sequence  
 283 <220> FEATURE:  
 284 <223> OTHER INFORMATION: 6873-6896 in JS95 sil, 5096-5119 in M1  
 286 <400> SEQUENCE: 22

20  
 Insufficient explanation.  
 What is the source of P/s  
 genetic material?  
 See glem // on error  
 summary sheet. 22

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DATE: 06/29/2006

TIME: 10:17:34

Input Set : A:\73975\_SEQLIST.txt

Output Set: N:\CRF4\06292006\J525178.raw

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287 tcgatatgga gataaagaaa ctgg                                24
290 <210> SEQ ID NO: 23
291 <211> LENGTH: 22
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
296 <223> OTHER INFORMATION: 6804-6825 in M1 section 36
298 <400> SEQUENCE: 23
299 aacagtgcctt tcaggaactc ct                                22
302 <210> SEQ ID NO: 24
303 <211> LENGTH: 22
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: 10031-10052 in M1 section 36
310 <400> SEQUENCE: 24
311 ctaggtgcaa ttgaggagtc aa                                22
314 <210> SEQ ID NO: 25
315 <211> LENGTH: 20
316 <212> TYPE: DNA
317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
320 <223> OTHER INFORMATION: 20-43 in JS95 sil, 7287-7306 section 152 in M1
322 <400> SEQUENCE: 25
323 tcctcgcaact gttccaatag                                20
326 <210> SEQ ID NO: 26
327 <211> LENGTH: 20
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: 3580-3599 in M1 section 36
334 <400> SEQUENCE: 26
335 aggtggtggt ggagcaggta                                20
338 <210> SEQ ID NO: 27
339 <211> LENGTH: 21
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial Sequence
343 <220> FEATURE:
344 <223> OTHER INFORMATION: 1545-1565 in M1 section 36
346 <400> SEQUENCE: 27
347 aagaagtggc cccaatttct g                                21
350 <210> SEQ ID NO: 28
351 <211> LENGTH: 30
352 <212> TYPE: DNA
353 <213> ORGANISM: Artificial Sequence
355 <220> FEATURE:
356 <223> OTHER INFORMATION: Forward all M primer with BamHI site
358 <400> SEQUENCE: 28
359 cctgaaaatg aggatccttc ctaaaaaacg                        30

```

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/525,178

DATE: 06/29/2006

TIME: 10:17:35

Input Set : A:\73975\_SEQLIST.txt

Output Set: N:\CRF4\06292006\J525178.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date